Protein Purification (Ni-NTA His-Tag) Experiment Template

Structured Documentation for Recombinant Protein Production — From Culture Harvest Through Affinity Chromatography and SDS-PAGE-Validated Yield and Purity

Applies to

- Academic and structural-biology research laboratories
- Biotechnology and pharmaceutical R&D groups
- Protein-production groups and core facilities
- Contract research organizations (CROs)

Relevant compliance & integrity frameworks

- **FDA 21 CFR Part 11** — Electronic records and signatures
- **GLP** — Good Laboratory Practice for preclinical documentation
- **Data integrity (ALCOA+)** — Attributable, contemporaneous, defensible records
- **NIH / NSF** — Reproducibility and data-management requirements

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1. Executive Summary

In recombinant protein work, the prep result is decision data. The yield in milligrams, the concentration, and the purity a purification delivers determine whether a construct is usable for crystallography, a biophysical assay, or antibody production — and whether a project scales the prep up or re-engineers the construct. But a yield number is only as trustworthy as the expression, the capture, the wash stringency, and the QC behind it. A protein reported as “pure” with no SDS-PAGE call or A280 trace behind it is not a weak result — it is an unverifiable one. A wash that is too gentle carries contaminants into the pool; one that is too harsh strips the target off the resin. And when per-fraction A280 readings, gel images, and yields live scattered across UNICORN files, shared drives, and notebooks, purification outcomes cannot be compared reliably across constructs and preps — which is the entire point of a protein-production effort.

The ELabELN Protein Purification (Ni-NTA His-Tag) Experiment Template solves this by providing a pre-built, fully structured prep record that loads from the template library in a single click. It ships with a 10-step Ni-NTA affinity protocol, validated buffer references, pre-wired expression and yield-QC fields, and typed inputs for expression host, construct, induction conditions, lysis method, column type, imidazole gradient steps, A280 elution peak, eluate volume, eluate concentration, total yield, purity, and identity verification. The expression vector, induction reagents, lysis buffers, HisTrap column, and SDS-PAGE reagents link to the ELabELN inventory, and the tamper-evident audit trail captures every culture, every prep run, and every QC decision.

This white paper describes what the template contains, the recombinant-protein use case it is designed to support, the upstream and downstream workflows it connects to, the benefits it delivers to the scientist, and how a laboratory can deploy it and begin running purifications within days.

> **Key benefit**
> Labs that adopt the Protein Purification template stop rebuilding the buffer setup every prep and lose no fraction, A280 reading, or gel call between the FPLC and the notebook. Purity is gated by SDS-PAGE, every yield carries its chromatography and QC, and outcomes become queryable across a construct’s prep history — the structured, comparable foundation a real protein-production campaign and defensible material provenance depend on.

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2. What Is His-Tag Affinity Purification, and Why Does Documentation Matter?

2.1 The Technique

His-tag affinity purification exploits the affinity of a polyhistidine tag, engineered onto a recombinant protein, for immobilized nickel ions. Cells expressing the tagged protein are harvested and lysed, the lysate is clarified, and the cleared load is passed over a Ni-NTA (immobilized-metal affinity) column: the tagged protein binds while most host proteins flow through. Low concentrations of imidazole wash weakly bound contaminants away, and a higher imidazole concentration then competes the tagged protein off the resin. On an FPLC, absorbance at 280 nm (A280) monitors protein in the eluate in real time, so the elution peak can be collected as discrete fractions, quantified by A280 or a Bradford assay, and assessed for purity by SDS-PAGE. The prep is described by its total yield (mg), concentration (mg/mL), and purity (percent by densitometry), together with confirmation of the protein's identity.

A yield or purity number is only meaningful if the whole chain performed: good expression and solubility, efficient capture on the column, washes stringent enough to remove contaminants but not the target, a clean elution collected at the right fractions, and a validated gel to confirm it. Weakness anywhere in that chain produces a protein that looks pure and is not, or a yield that cannot be reproduced in the next prep.

Because the purified material advances into structure determination, assays, or scale-up and is compared across constructs and preps, **the chromatography trace, the per-fraction data, the yield, and the SDS-PAGE purity are what make a prep trustworthy and comparable to the next one — which is exactly why they must live in one structured, queryable record rather than a folder of UNICORN files and gel images.**

2.2 The Documentation Problem

Recording purifications across instrument files, gel images, and paper notebooks creates a set of interconnected risks:

- Buffer recipes and imidazole gradients are rebuilt by hand each prep, so an inconsistent wash quietly makes purity non-comparable across constructs.
- The FPLC chromatogram sits in a UNICORN file, disconnected from the construct, culture, and yield it describes.
- Per-fraction A280 readings, volumes, and pooling decisions live in a scratch spreadsheet or on paper, unlinked to the prep record.
- The SDS-PAGE gel image is saved to a shared drive, and the purity call is remembered rather than recorded against the prep.
- Yield, concentration, and purity are noted inconsistently, so cross-prep trends for a construct cannot be queried.
- Column and reagent lots and column-use history are not captured, so a drop in performance cannot be traced to a resin or buffer batch.
- Prior preps of the same construct cannot be retrieved to compare, so scale-up and re-engineering decisions rest on memory.

These are the gaps that make purification data hard to trust and compare, and they are the gaps this template was designed to close.

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3. Template Overview: What Ships with the Template

The ELabELN Protein Purification (Ni-NTA His-Tag) Experiment Template is a pre-populated experiment record available to all ELabELN subscribers directly from the template library. It ships configured for Ni-NTA affinity purification of a His6-MBP-GFP fusion (~72 kDa) from a 1 L IPTG-induced E. coli BL21(DE3) culture, with a 10-step protocol covering harvest through SDS-PAGE-validated eluate. The default protocol assumes a 5 mL HisTrap HP column on an ÄKTA pure FPLC, a 4-step imidazole gradient (10 mM equilibration, 20 mM wash, 50 mM wash, 250 mM elution) at 1 mL/min with A280 monitoring, fraction collection of the elution peak, a Bradford assay for quantitation, and SDS-PAGE for purity assessment. Every section is editable — the configuration is a tested baseline, not a locked format.

3.1 Template Sections at a Glance

The template populates the existing ELabELN experiment sections your lab already works in. Your team edits a working baseline instead of rebuilding the buffer setup from scratch every prep.

Section	What it pre-populates
Main Text	Prep design, construct notes, and the expected yield and purity, authored in the TinyMCE rich-text editor and linked to the upstream expression culture.
Extra Fields	Twelve structured, typed fields grouped as Expression, Lysis & Capture, and Elution & QC — host, construct, induction conditions, lysis method, column type, imidazole gradient steps, A280 elution peak, eluate volume, eluate concentration, total yield, purity, and identity verification. Typed values make purification outcomes queryable across preps.
Steps	A 10-step workflow checklist covering harvest through SDS-PAGE QC. Each tick is timestamped to the audit trail, and the FPLC run is auto-logged.
Compounds	The expression vector, IPTG, lysis buffer, HisTrap column, imidazole, and SDS-PAGE reagents pre-linked from the compound database, with the column lot carried in automatically and buffer recipes shown inline.
Links & Resources	Pre-wired to the lab's His-tag Purification SOP v2.3, the pET-MBP-GFP construct sequence map, and prior preps of the same construct.
Storage & Files	−80 °C glycerol-stock and purified-protein storage, plus labelled attachment slots for FPLC chromatograms (PNG) and ÄKTA UNICORN method files.

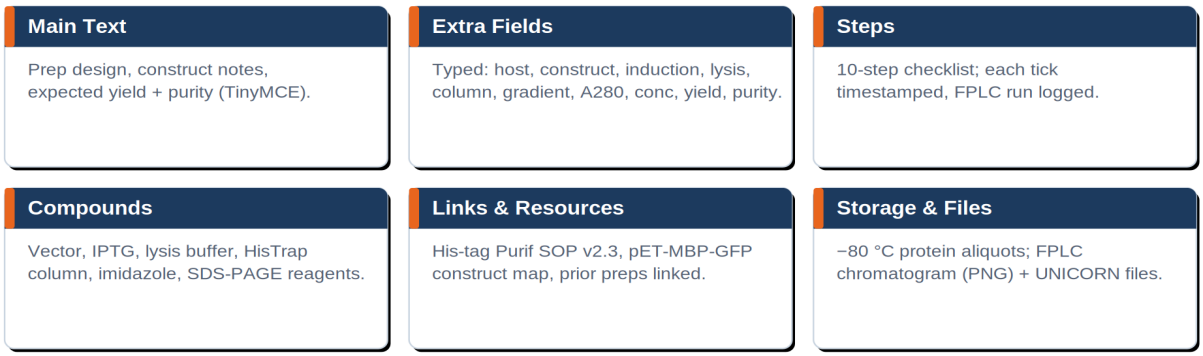

Figure 1. The six ELabELN experiment sections pre-populated by the Protein Purification (Ni-NTA His-Tag) template.

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3.2 The 10-Step Protocol

The workflow checklist is the operational spine of the template. Each step maps to a discrete bench or analysis action and writes a timestamped, user-attributed entry to the audit trail when checked off. The FPLC run is auto-logged, and the chromatography data and SDS-PAGE densitometry are captured from the instrument and gel-analysis tools, with the resulting values recorded as typed fields.

Step	Action	What it captures
1	Harvest culture (1 L BL21)	Expression host; induction; culture volume
2	Lyse cells (sonication)	Lysis method; lysis buffer
3	Clarify lysate (centrifuge)	Cleared load
4	Equilibrate & load HisTrap	Column type; equilibration (10 mM)
5	Wash (20 mM imidazole)	Wash stringency
6	Wash (50 mM imidazole)	Contaminant removal
7	Elute (250 mM imidazole)	A280 elution peak (FPLC)
8	Collect fractions	Fraction volumes; per-fraction A280
9	Bradford quantitation	Concentration; total yield
10	SDS-PAGE purity	Purity (% densitometry); identity; e-signature

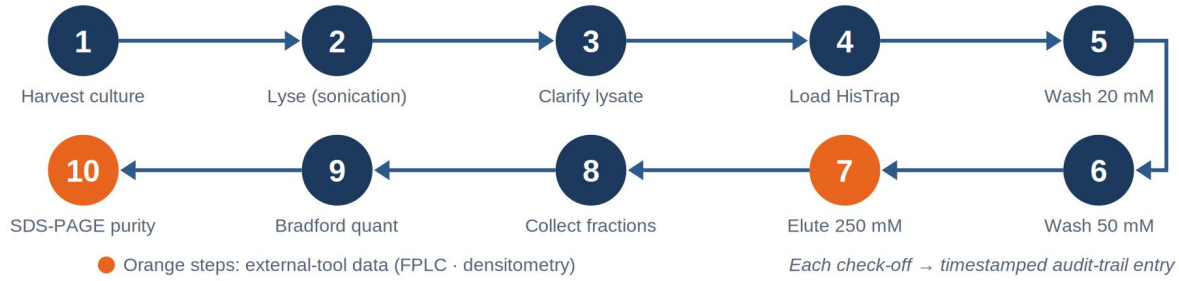

Figure 2. The 10-step Ni-NTA purification workflow — orange steps produce data captured from external tools (the ÄKTA UNICORN FPLC and SDS-PAGE densitometry); every check-off writes a timestamped entry to the ELabELN audit trail.

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4. The Use Case: When and How the Template Is Used

The template is intended as a tested baseline for academic, biotechnology, and pharmaceutical research labs producing recombinant proteins. It is configured around a recognizable reference — a His6-MBP-GFP Ni-NTA prep — but the scenarios it serves span the purification bench and the protein-production campaign it feeds.

4.1 Recombinant Protein Production (Primary Use Case)

The core scenario: producing purified protein for a downstream application. The template captures the chromatography, every fraction, the yield, and the SDS-PAGE purity in one structured record, so a prep is fully reconstructable — which construct, which column and gradient, which fractions, which purity — rather than a tube in the freezer detached from the run that produced it.

4.2 Construct and Affinity-Tag Screening

Early production work asks which construct and tag express well and purify cleanly. Because each prep's parameters are structured and queryable, expressing, soluble, and well-behaved constructs are triaged directly from the records rather than reconstructed from scattered files, and each outcome is linked to the culture and chromatography that justify it.

4.3 Expression and Solubility Optimization

Yield often turns on induction and lysis conditions. Because host, induction, lysis method, and the resulting yield and purity are all typed fields, the template makes it straightforward to compare conditions across preps and see which combination gives the best soluble yield for a given construct.

4.4 Multi-Step Purification and Polishing

Many targets need a polishing step after affinity capture. Because the record structures the affinity step and its outputs, it extends naturally to multi-step schemes — affinity followed by size-exclusion or ion-exchange — with each stage's chromatography and QC captured in the same prep record.

4.5 Yield and Purity QC Across Preps

Because yield, concentration, and purity are typed and queryable, the template doubles as a running production-QC record. A team can pull every prep of a construct, compare yields and purities side by side, and flag a prep whose gel call undermines its material — before questionable protein is carried into an assay.

4.6 Multi-PI Consortium and Core-Facility Collaboration

Protein production is often shared across labs and core facilities. Because every ELabELN edition includes unlimited users, the PI, scientists, and core staff can all work from the same records. Granular permissions let project leads control who can edit prep records versus only review them — important during the multi-PI consortium work that structural and biophysical projects frequently involve.

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5. Dependencies and Connected Workflows

The Protein Purification template does not exist in isolation. It sits inside a network of connected workflows — upstream, parallel, external, and downstream — that give the prep record its full scientific and decision-making value.

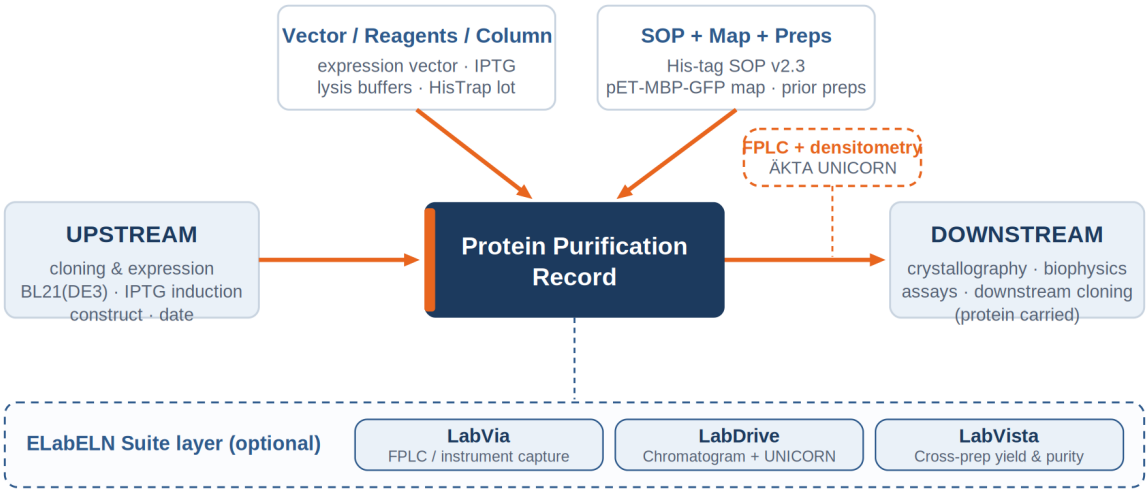

Figure 3. The template connects an upstream cloning and expression workflow, parallel inventory and SOP/construct-map/prior-prep systems, the external FPLC and gel-analysis tools, and downstream structure, biophysics, assay, and cloning workflows.

5.1 Upstream: Cloning, Expression, and Induction

Every purification begins with a cloned construct, an expression host, and an induced culture. The template links to the upstream expression workflow, so opening a prep surfaces the construct, the host and induction conditions, the operator, and the date — connecting each yield to the culture that produced it.

5.2 Parallel: Vector, Reagent, Column, and Buffer Inventory

The Compounds section links the expression vector, IPTG, lysis buffers, the HisTrap column, imidazole, and SDS-PAGE reagents directly to the ELabELN inventory. Because reagent identity and column condition bear on the prep result, this traceability is decisive. Through the link the record automatically carries:

- **Column and reagent lots and column-use history** so a drop in binding capacity or a shift in yield can be traced to a resin or buffer batch.
- **Buffer recipes, shown inline**, so the exact lysis, wash, and elution conditions are on the record and reproducible.
- **Expiry and stock levels**, with low-stock warnings before a run, so a prep is not started against a depleted or expired reagent.

Barcode and QR scanning can populate these links from the physical vial or column, keeping lot capture effortless across a prep.

5.3 Parallel: SOPs, the Construct Map, and Prior Preps

The Links section connects the prep to the lab's His-tag Purification SOP, the construct sequence map, and prior preps of the same construct. That last link is what turns individual

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preps into a campaign: each new prep opens alongside the construct's history, so the yield and purity trend is built in rather than reconstructed.

5.4 External: The FPLC and Gel-Analysis Tools

The chromatography runs on the FPLC, and purity is assessed on a gel and quantified by densitometry. ELabELN is the system of record around those tools: the full per-fraction matrix (fraction, volume, A280, concentration, and SDS-PAGE call) lives in the spreadsheet editor, the FPLC chromatogram and ÄKTA UNICORN method files attach in the Storage & Files section, and the yield, concentration, and purity are written back into the typed Elution & QC fields. Direct FPLC data import (ÄKTA, NGC) is available through the optional ELabELN instrument-integration plugin; the chromatography evidence and the reported yield stay together in one record either way.

5.5 Downstream: Structure, Biophysics, Assays, and Cloning

The purified protein feeds crystallography and cryo-EM, biophysical characterization, functional and binding assays, antibody production, and downstream cloning — and, because yield and purity are typed and queryable, cross-prep and cross-construct comparison. A scale-up or re-engineering decision rests on a documented, comparable production history rather than a number recalled from memory.

5.6 The ELabELN Suite: Instruments and Dashboards

Everything above is available in ELabELN Standard. Labs on the ELabELN Suite gain three layers that connect to the same record: LabVia captures data directly from the FPLC and other instruments; LabDrive adds metadata search, versioning, and role-based access across chromatogram and UNICORN-file archives; and LabVista builds cross-prep yield and purity dashboards on the structured purification metadata. The same audit trail and data-integrity controls span all layers.

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6. How the Scientist Benefits

The template is built to deliver value at the bench and to the campaign alike. The benefits compound with every prep a lab runs.

6.1 Start From a Tested Baseline, Not a Blank Buffer Setup

The scaffold — protocol, typed fields, buffer setup, column and reagent links, SOP, and construct-history link — is already built. The scientist edits a working configuration to match the construct and host they actually purify, rather than rebuilding the buffer setup from scratch every prep. The first prep is faster, and every subsequent one is consistent and comparable.

6.2 Document by Doing

Checking off each of the 10 steps as it happens produces a contemporaneous, timestamped record as a by-product of the prep, and the FPLC run is auto-logged. There is no separate write-up to reconstruct later.

6.3 Never Lose Chromatography or Fraction Provenance Again

Because the per-fraction matrix is a structured artifact and the column and reagents are linked to inventory, the chromatogram, fraction data, lots, and QC are captured permanently on every prep. When a yield or purity is questioned, the chromatography and its provenance are on the record — closing the most common purification troubleshooting gap by default.

6.4 Cross-Construct Yield and Purity You Can Query

Typed yield, concentration, and purity fields make the campaign queryable. A team can pull every prep of a construct, trend yield and purity prep by prep, and gate on the gel call at a glance — turning a folder of UNICORN files and gel images into a live production view.

6.5 Purity Gating and Defensible Material Provenance

Capturing the SDS-PAGE purity beside every yield makes material quality a visible, queryable gate rather than an afterthought, and the tamper-evident audit trail, column and reagent traceability, and electronic signatures give each batch of purified protein a defensible provenance — structured to support FDA 21 CFR Part 11 review and GLP-relevant documentation when the lab's quality system requires it.

> **At the bench, in practice**
>
> A scientist opens the template, sets the construct and host to match today's prep, scans the column and reagent vials to capture their lots, and checks off each step as the culture is harvested, lysed, loaded, washed, and eluted. The FPLC A280 populates the fraction table; the gel is imaged, and the purity call and yield go into typed fields — the SDS-PAGE confirming the material was worth carrying forward. Weeks later, comparing the construct's history, the PI queries every prep and watches yield and purity trend, prep by validated prep.

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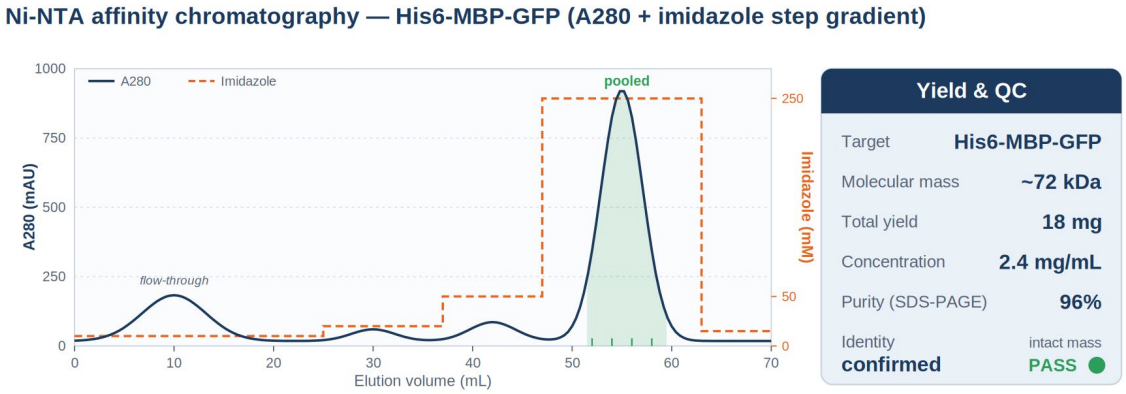
7. The Chromatogram and Prep Quality

7.1 The Default Reference: A His6-MBP-GFP Ni-NTA Prep

The template ships configured for a Ni-NTA affinity prep of a His6-MBP-GFP fusion (~72 kDa) from a 1 L IPTG-induced E. coli BL21(DE3) culture: sonication lysis, a clarified load onto a 5 mL HisTrap HP column, and a 4-step imidazole gradient in which unbound protein flows through, 20 mM and 50 mM washes remove contaminants, and a 250 mM step elutes the target as a sharp A280 peak. The peak is collected as fractions, the pool is quantified, and SDS-PAGE confirms purity and identity. This concrete reference demonstrates the full harvest-to-QC workflow out of the box; swap the host, construct, affinity tag, or chromatography to match what your lab purifies.



Illustrative — A280 trace, imidazole gradient and per-fraction data are captured in ELabELN; yield, concentration and SDS-PAGE purity recorded as typed fields.

Figure 4. A Ni-NTA affinity chromatogram — the A280 trace and imidazole step gradient with the pooled elution fractions marked — alongside the yield-and-QC panel (with SDS-PAGE purity confirming the material). Illustrative; the trace and per-fraction data are captured in ELabELN, and yield, concentration, and purity are recorded as typed fields.

7.2 How the Template Handles the Chromatogram, Fractions, and Purity

The full per-fraction matrix — fraction, volume, A280, concentration, and SDS-PAGE call (clean / contaminated / discarded) — lives in the spreadsheet editor, structured for direct pooling and quality decisions. The FPLC chromatogram and ÄKTA UNICORN method files attach in the Storage & Files section, and the total yield, eluate concentration, and purity (percent by densitometry) are written back into the typed Elution & QC fields. Because these values are structured and queryable, cross-prep comparison is straightforward: query every prep of a construct, gate on the gel call, and review yield and purity side by side — the production view a campaign runs on. Direct FPLC data import (ÄKTA, NGC) is available through the optional ELabELN instrument-integration plugin.

Element	Default configuration	Editable to
Expression host	E. coli BL21(DE3)	Insect (Sf9 / Hi5), mammalian (HEK293 / CHO)
Construct / tag	His6-MBP-GFP fusion	His10, GST, MBP, Strep, FLAG, SUMO
Lysis method	Sonication	French press, microfluidizer, detergent

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Element	Default configuration	Editable to
Chromatography	Ni-NTA (HisTrap HP) on FPLC	GSH-Sepharose, Strep-Tactin, amylose, anti-FLAG
Gradient / elution	4-step imidazole, 10–250 mM	Linear or step; any range
Scheme	Single-step affinity	Multi-step (affinity + SEC / ion exchange)

Figure 5. The template's default configuration — fully editable for any host, construct, affinity tag, chromatography, or purification scheme.

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8. Configuring the Template for Your Prep

Adapting the template to a different construct or chromatography is a matter of editing the relevant sections — not rebuilding the structure.

8.1 Swap the Host and Construct

Change the expression host — E. coli, insect Sf9/Hi5, or mammalian HEK293/CHO — and the construct by editing the Expression section. If the vector and reagents already exist in the ELabELN compound database, simply re-link them; their lots and recipes flow in automatically.

8.2 Change the Affinity Tag and Chromatography

Switch the affinity tag and matching resin — His6/His10 on Ni-NTA, GST on GSH-Sepharose, Strep on Strep-Tactin, MBP on amylose, or FLAG on anti-FLAG — by editing the Lysis & Capture section. The per-fraction matrix and QC fields apply regardless of the affinity chemistry.

8.3 Adjust Lysis, Gradient, and Single- vs. Multi-Step

Change the lysis method (sonication, French press, microfluidizer, detergent), tune the imidazole gradient, and move from a single-step affinity capture to a multi-step scheme (affinity plus size-exclusion or ion-exchange) by editing the chromatography section. The record structures each stage the same way.

8.4 Save a Custom Version

Once configured, save your edits as a private template scoped to your lab, or publish back to the ELabELN template library. Every subsequent prep opens from your configured baseline, and separate versions can be maintained for different constructs, tags, or purification schemes.

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9. Getting Started

ELabELN Standard is a cloud-hosted SaaS deployment typically live within one to two business days of account creation. There is no hardware to buy, no IT project, and no per-seat licensing.

1. **Start an ELabELN account.** Visit elabeln.com/get-started. ELabELN Standard runs on LabLynx's managed cloud infrastructure.
2. **Provision your instance.** LabLynx provisions the instance within one to two business days; you receive a URL, admin credentials, and onboarding documentation.
3. **Load the Protein Purification template.** From the template library, select the Protein Purification (Ni-NTA His-Tag) template and click "Use This Template." An editable instance opens immediately.
4. **Add your construct, reagents, and column to the inventory.** Enter your expression vector, induction reagents, lysis buffers, HisTrap column, imidazole, and SDS-PAGE reagents with lot numbers and storage locations. This is a one-time setup step.
5. **Link your SOP, construct map, and prior preps.** Upload your His-tag purification SOP and construct sequence map, and connect prior preps of the construct to the template's Links section.
6. **Customize the template for your prep.** Edit the host, construct, affinity tag, lysis method, and imidazole gradient, then save as a private team version.
7. **Run your first prep.** Open your saved template, complete the 10-step checklist, capture the chromatogram and per-fraction data, record the yield and purity, attach the UNICORN file and gel image, and sign off.

> **Typical timeline**
> Day 1: Account requested at elabeln.com/get-started. Day 2–3: Instance provisioned; construct, reagent, and column inventory populated; SOP, construct map, and prior preps linked. Day 3–4: Template configured and saved as a private version for your construct and host. Day 4–5: First prep documented in ELabELN with the chromatogram, per-fraction data, yield, and purity captured and an e-signature.

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9.1 ELabELN Standard vs. ELabELN Suite

Capability	Standard	Suite
Protein Purification template access	Included	Included
Unlimited users	Included	Included
Audit trail and e-signatures	Included	Included
Vector / reagent / column inventory with lot tracking	Included	Included
SOP, construct-map & prior-prep linking	Included	Included
Per-fraction matrix + chromatogram / UNICORN attachments	Included	Included
LabVia direct FPLC / instrument capture	—	Suite layer
LabDrive chromatogram & UNICORN archive search & versioning	—	Suite layer
LabVista cross-prep yield & purity dashboards	—	Suite layer

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10. Frequently Asked Questions

Can I configure the template for my construct and host?

Yes. Every section is editable. Swap in different expression hosts (E. coli, insect Sf9/Hi5, mammalian HEK293/CHO), change the construct and affinity tag (His6, His10, GST, MBP, Strep, FLAG, SUMO), adjust the lysis method (sonication, French press, microfluidizer, detergent), change the chromatography (Ni-NTA, GSH-Sepharose, Strep-Tactin, amylose, anti-FLAG), or move from single-step affinity to multi-step (affinity + SEC, ion exchange). Save your edits as a private template scoped to your lab, or publish back to the ELabELN template library.

Does the template support FPLC integration?

The template captures the FPLC method-file reference, A280 elution-peak retention, fraction volumes, and pooled-fraction concentration in typed fields. ÄKTA UNICORN method files and chromatograms attach via the Storage & Files section, and the spreadsheet editor captures per-fraction QC for cross-prep tracking. Direct FPLC data import (ÄKTA, NGC) requires the optional ELabELN instrument-integration plugin.

Does the template track yield and purity across constructs?

Yes. The typed Elution & QC group holds total yield (mg), eluate concentration (mg/mL), and purity (percent by SDS-PAGE densitometry), all queryable across the construct's prep history. Combined with the upstream expression notes, your lab can pull every prep for a given construct and see how expression and purification yields trend, supporting decisions about scale-up or construct re-engineering.

Is it included in every ELabELN plan?

Yes. Every published template in the ELabELN library is available to all subscribers in both the Standard and Suite editions, with unlimited users in either edition and no per-template fee.

Can my whole lab use this template?

Yes. Every ELabELN edition includes unlimited users, so the PI, postdocs, grad students, rotating researchers, and core-facility staff can all use the template without per-seat charges. Granular permissions let project leads control who can edit prep records versus only review them.

How quickly can my lab start running purifications in ELabELN?

ELabELN Standard cloud deployment is typically live in one to two business days. Once the instance is provisioned, the template loads from the library in a single click, with the construct, host, tag, and chromatography editable to match the preps your lab actually runs.

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11. Conclusion

The ELabELN Protein Purification (Ni-NTA His-Tag) Experiment Template is not simply a digital version of a UNICORN file. It is a structured, audit-ready, searchable record that connects to your vector, reagent, and column inventory, your SOPs and construct maps, the expression culture the prep followed, your FPLC and gel-analysis tools, and the structure, biophysics, assay, and cloning workflows the purified protein feeds — and, in the Suite edition, cross-prep yield and purity dashboards. It turns a purification into a record whose chromatography, prep quality, and yield are captured, comparable, and defensible.

For a laboratory that runs purifications regularly, the benefit compounds with every campaign. Chromatograms, fraction data, and yields accumulate into one queryable production history. Every column and reagent lot is traceable. Every prep is gated by its SDS-PAGE purity, and every batch of protein carries a defensible provenance — so material of uncertain purity can no longer quietly enter an assay, and the yield and purity trend that guides scale-up is built in rather than reconstructed.

The template is available to all ELabELN subscribers today. A new instance is live in one to two business days, and the first structured prep is typically documented within a week of account creation.

> **Get started**
> Visit elabeln.com/get-started to request your ELabELN instance, or contact LabLynx at 866.522.5969 or info@lablynx.com. Load the Protein Purification (Ni-NTA His-Tag) template, configure it for your construct and host, and run your next prep from a tested, audit-ready baseline.

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